



# ***ABRF Studien***

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***Association of  
Biomolecular Resource  
Facilities***



# *Was ist ABRF?*

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- **Non-Profit Gesellschaft**
  - **140 Cores**
  - **Biotechnologische Labors**
  
- **Academia, Industrie, Gerätehersteller**
  
- **Breites Spektrum biomolekularer Technologien**
  - **Protein, DNA, Metaboliten, Mikroskopie, etc.**
  
- **Forschung, Technologie, Kommunikation**
  - **Konferenzen, Journal, Listserv, Research Group Studien**



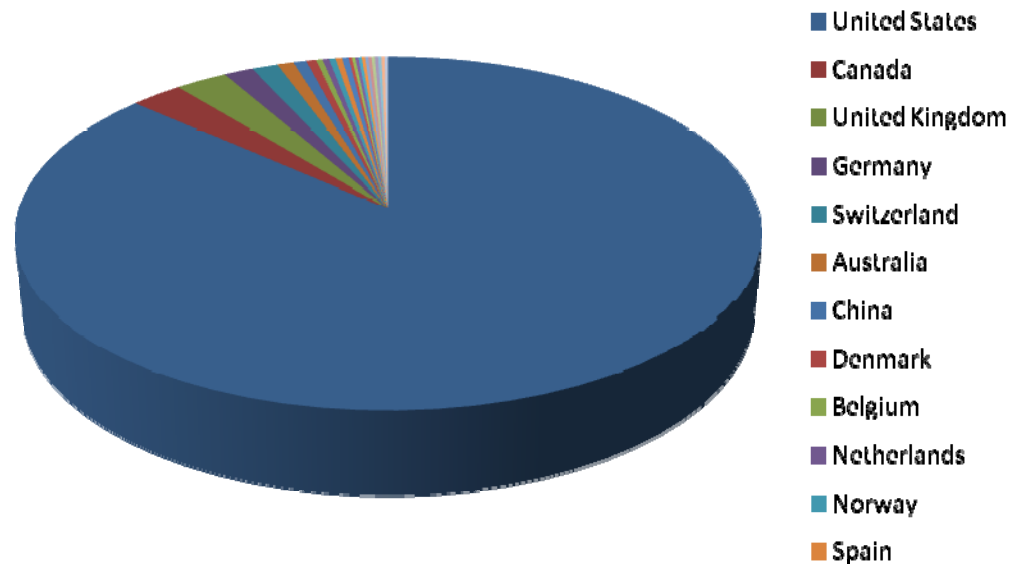
# *Mitgliedschaft*

**600 – 800 Mitglieder**

**463 Akademischer Bereich**

**153 Firmen**

**ca. 1.000 Teilnehmer bei den alljährlichen Konferenzen**





# *Konferenz*

**ABRF**  
**2012**

**LEARNING FROM BIOMOLECULES**  
**THE TECHNOLOGY BEHIND THE STORY**

March 17-20, 2012

Disney's Contemporary Resort, Orlando, Florida

*An International Symposium of the Association of Biomolecular Resource Facilities*



# *Konferenz – Satellite Courses*

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- **Introduction to Proteomics Platforms: Qualitative and Quantitative Studies**
- **Targeted Proteomics**
- **An Introduction to Metabolomics**
- **RNA Demystified for Laboratories**
- **Next Generation Sequencing Considerations For Core Professionals**
- **Managing Performance and Productivity in the Laboratory**
- **Lean Management in Core Facilities**



# Kommunikation - Listserv



E-mail Diskussionsforum

Frei für jederman zugänglich!

## ABRF Web-Based Discussion Forum

[\[ Information \]](#) [\[ Archives Home \]](#)

[\[ Join Group \]](#) [\[ Sign In \]](#)

Date Range: Last 7 Days Show: 50 per page  
From: Sep 8 2010 To: Sep 15 2010  
Sort By: Thread Search Archives  
Keyword(s):  
(Optional) Find:  All  Any  Phrase  Advanced  
Find in:  Anywhere  Subject  Author

Message Index (30 messages found) 30801 messages in archive

Subject	From	Received On (local time)
<a href="#">New submission to the DSRG Sequencing Troubleshooting Web Resource</a>	zianni.1@osu.edu	14-Sep-10 22:31 (GMT -4)
<a href="#">New submission to the DSRG Sequencing Troubleshooting Web Resource</a>	zianni.1@osu.edu	14-Sep-10 22:14 (GMT -4)
<a href="#">MALDI MS for peptide ~1000</a>	jy2344@columbia.edu	14-Sep-10 17:20 (GMT -4)
<a href="#">Re: MALDI MS for peptide ~1000</a>	Bruce Stanley	14-Sep-10 17:43 (GMT -4)
<a href="#">MS MALDI Waters Repair</a>	eqk3@psu.edu	13-Sep-10 15:48 (GMT -4)
<a href="#">Trouble with Phosphopeptides on anal.HPLC</a>	peptides@kinexus.ca	8-Sep-10 11:29 (GMT -4)
<a href="#">Re: Trouble with Phosphopeptides on anal.HPLC</a>	Richard F Cook	8-Sep-10 13:23 (GMT -4)
<a href="#">AW: Trouble with Phosphopeptides on anal.HPLC</a>	Mechtler, Karl	13-Sep-10 2:19 (GMT -4)
<a href="#">Re: AW: Trouble with Phosphopeptides on anal.HPLC</a>	Amos Heckendorf	13-Sep-10 12:14 (GMT -4)
<a href="#">Small RNA Agilent chips</a>	Deb Grove	10-Sep-10 11:14 (GMT -4)
<a href="#">Information Technology Session at ABRF 2008</a>	Laurey Steinke	8-Sep-10 15:20 (GMT -4)
<a href="#">Re: Information Technology Session at ABRF 2008</a>	Scottie Adams	8-Sep-10 15:46 (GMT -4)



# *Resources*

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- [White Pages](#)
- [Yellow Pages](#)
- [Site Search](#)
- [Delta Mass](#)
- [DNA Sequencing Troubleshooting Resource](#)
- [Authorship Guidelines](#)
- [Research Group and Committee Guidelines](#)
- [ABRF Affiliates and Chapters - Operating Guidelines](#)
- [Request for support for external meeting](#)
- [Conflict of Interest form](#)
- [ABRF Travel Reimbursement Forms](#)
- [Job Openings](#)
- [Site Help](#)



# Delta Mass

## Delta Mass

*A Database of Protein Post Translational Modifications*

### Search the Delta Mass Database [View All](#)

Enter a +/- integer to search on, and select a margin of error (range of search).

Avg. Mass Change:  Error Margin:

Avg. Mass Change	Modification
-79	5' dephospho
-58	Desmosine (from Lysine)
-48	<a href="#">decomposed carboxymethylated Methionine</a>
-44	<a href="#">decarboxylation of gamma carboxy Glutamate</a>
-43	<a href="#">gamma-glutamyl semialdehyde (from arginine)</a>
-42	Ornithine (from Arginine)
-34	Lysinoalanine (from Cysteine)
-34	<a href="#">Lanthionine (from Cysteine)</a>
-34	<a href="#">Dehydroalanine (from Cysteine)</a>
-30	Homoserine formed from Met by CNBr treatment
-27	<a href="#">Oxidation of arginine (to glutamic acid)</a>
-18	<a href="#">Formylglycine (from cysteine)</a>
-18	<a href="#">Pyroglutamic Acid formed from Glutamic Acid</a>
-18	Dehydration (-H <sub>2</sub> O)
-18	S-gamma-Glutamyl (crosslinked to Cysteine)
-18	O-gamma-Glutamyl- (Crosslink to Serine)
-18	Serine to Dehydroalanine
-18	Alaninohistidine (Serine crosslinked to theta or pi carbon of Histidine)
-18	<a href="#">Misincorporation of Norleucine for Methionine</a>



# *‘Core Facility’ Themen*

## **Von ABRF empfohlene Richtlinien zur Autorenschaft**

<http://www.abrf.org/index.cfm/page/reference/Authorship.htm>

**Important reasons for acknowledging contributions from core facilities in publications, by co-authorship or by formal mention in the acknowledgments section, include:**

1. Core facility personnel are scientists. When they make a substantial intellectual and/or experimental contribution to a publication they deserve to be acknowledged just as any other co-author.
2. The existence of core facilities depends in part on proper acknowledgment in publications. This is an important metric of the value of most core facilities. Proper acknowledgment of core facilities enables them to obtain financial and other support so that they may continue to provide their essential services in the best ways possible. It also helps core personnel to advance in their careers, adding to the overall health of the core facility.

**“Research Technologies: Fulfilling the Promise” Angeletti, Bonewald, de Jongh, Niece, Rush and Stults (1999) FASEB Journal 13:595**

**“A Framework for Managing Core Facilities within the Research Enterprise” Haley R (2009) Journal of Biomolecular Techniques, 20:226-230**



# *Affiliates and Chapters*

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Midwest Association  
of Core Directors

**MCBIOS.ORG**

MIDSOUTH COMPUTATIONAL BIOLOGY & BIOINFORMATICS SOCIETY



ASSOCIATION CANADIENNE DE CYTOMETRIE  
CANADIAN CYTOMETRY ASSOCIATION



# Chapter?



# www.abrf.org

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**The Association of Biomolecular Resource Facilities**

Research • Technology  
Communications • Education

ABRF Annual Meeting  
ABRF 2012  
March 17-20  
Orlando, FL

- About ABRF
- Membership
- Research Groups
- ABRF Resources
- Communications
- Meetings

## The ABRF is

The Association of Biomolecular Resource Facilities is an international society dedicated to advancing core and research biotechnology laboratories through research, communication, and education. [Learn more about us.](#)

## Connect to the World

The ABRF Electronic Discussion Forum

MAY 1, 2011, by Samuel Chun-lap Lo [ABCT]  
[Loss of resolution in the post-column derivatization module](#)

APR 29, 2011, by Jinhong Shi  
[Does ProteinProphet use any specific database to identify proteins?](#)

APR 29, 2011, by James Farmer  
[GC-MS of isopentenyl methyl sulfides](#)

## ABRF Publications



## News Headlines

Welcome to the Updated ABRF Website »

PRG 2008 2009 and 2010 studies now published in the journal "Proteomics." »

ABRF ex-President Jay Fox sought funding for ABRF at Capitol Hill »

Complex Carbohydrate Research Center - Training Courses »

[More ABRF News »](#)

## Research Groups

Advancing Core Technologies and Standards

ABRF Research Groups advance core biomolecular technologies by sponsoring research studies that help researchers and facilities evaluate analytical techniques and methodologies, as well as help establish good laboratory practices.

- Learn more about Research Groups
- Research Group Publications



## Corporate Sponsors



## Academic Sponsors



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ABRF Business and Membership Office  
9650 Rockville Pike, Bethesda, MD 20814  
(301) 834-7308 (phone) | (301) 834-7455 (fax)  
[abrf@abrf.org](mailto:abrf@abrf.org)

Site Design & Programming by [WebSite Concepts, Inc.](#)



# *ABRF Research Groups*

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## *Benchmarking für breites Spektrum biomolekularer Technologien*

**Antibody Technology (ARG)**

**DNA Sequencing (DSRG)**

**Genomic Variation (GVRG)**

**Glycoprotein (gPRG)**

**Light Microscopy (LMRG)**

**Metabolomics (MRG)**

**MicroArray (MARG)**

**Molecular Interactions (MIRG)**

**Nucleic Acids (NARG)**

**Protein Expression (PERG)**

**Protein Sequencing (PSRG)**

**Proteome Informatics (iPRG)**

**Proteomics (PRG)**

**Proteomics Standards (sPRG)**



# *Research Group Studien*

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- **Mechanismus zur Selbstevaluierung**
  
- **Verbesserung von Qualität und Methoden**
  - Routine und neue Technologien
  - Möglichkeiten und Limits
  
- **Zielgruppe**
  - Core Personal
  - Core Manager
  - Anwender
  
- **Wichtig**
  - Anonym
  - Kein Wettbewerb !!!



# *Proteomik Studien*

---

- **Evaluierung des Leistungsspektrums**
  - **Benchmarking**
- **Relevanz**
  - **Gegenwärtiger Stand der Technik und Routine Praxis**
  - **Evaluierung neuer Ansätze**
- **Präsentation auf ABRF Konferenz**
  - **Erfolgreiche Ansätze**
- **Veröffentlichung**
  - **Proteomik Journale**
  - **Website**



## *xPRG Studien*

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- **Bisher 20 Studien durchgeführt.**
- **Publiziert und auf Konferenzen präsentiert.**
- **In Proteomics Journalen kommentiert.**
- **Präsentationsfolien, Poster und Teilnehmer Protokolle sind auf den PRG/sPRG/iPRG/gPRG Websites für alle einsehbar.**



# *xPRG Mitglieder*

## **PRG:**

Tracy M. Andacht  
David Arnott  
Keiryn Bennett  
Maureen Bungler  
Cory Bystrom  
Allis S. Chien  
Larry Dangott  
Arnold M. Falick  
David B. Friedman  
Mary A. Gawinowicz  
Raymond Grant  
David Hawke  
Jeffrey Kowalak  
Jeroen Krijgsveld  
William S. Lane  
John Leszyk

Kathryn S. Lilley  
Michael MacCoss  
Henrik Molina  
Robert L. Moritz  
Thomas Neubert  
Len Packman  
Brett S. Phinney  
Robert E. Settlege  
Nicholas Sherman  
Kaye D. Speicher  
Kathy Stone  
Chris W. Turck  
Susan Weintraub  
Karen A. West  
H. Ewa Witkowska  
Nathan A. Yates

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David Arnott  
Christopher Colangelo  
Craig Dufresne  
Jim G. Farmar  
Mary A. Gawinowicz  
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Christopher R. Kinsinger  
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Rachel Loo  
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Brett S. Phinney  
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Kristie Rose  
Scott Shaffer  
Steve E. Stein  
Susan Weintraub

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Nuno Bandera  
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Brian C. Searle  
Sean L. Seymour  
David L. Tabb

## **gPRG:**

Wolfgang Egge-Jacobsen  
Karen R. Jonscher  
Rodney Keck  
Daniel Kolarich  
Ron Orlando  
Joseph Zaia



# *PRG Studien*

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- **PRG2011:** The Big Survey
- **PRG2010:** Identifying unanticipated problems in an otherwise straightforward analysis
- **PRG2009:** A targeted relative protein quantification study relevant for a biomarker validation project
- **PRG2008:** Identify differences between two samples that have different lengths of the same protein sequence
- **PRG2007:** Relative abundance of 12 proteins spiked into an *E. coli* lysate
- **PRG2006:** Relative abundance of 8 proteins between 2 different samples
- **PRG2005:** Sequencing Unknown Peptides
- **PRG2004:** Differentiation of Protein Isoforms
- **PRG2003:** Phosphorylation Site Determination
- **PRG2002:** Identification of Proteins in a Simple Mixture



# *PRG2006 Research Study*

## *Relative Quantifizierung*

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# *PRG2006 Relative Quantifizierung*

## *Ziele*

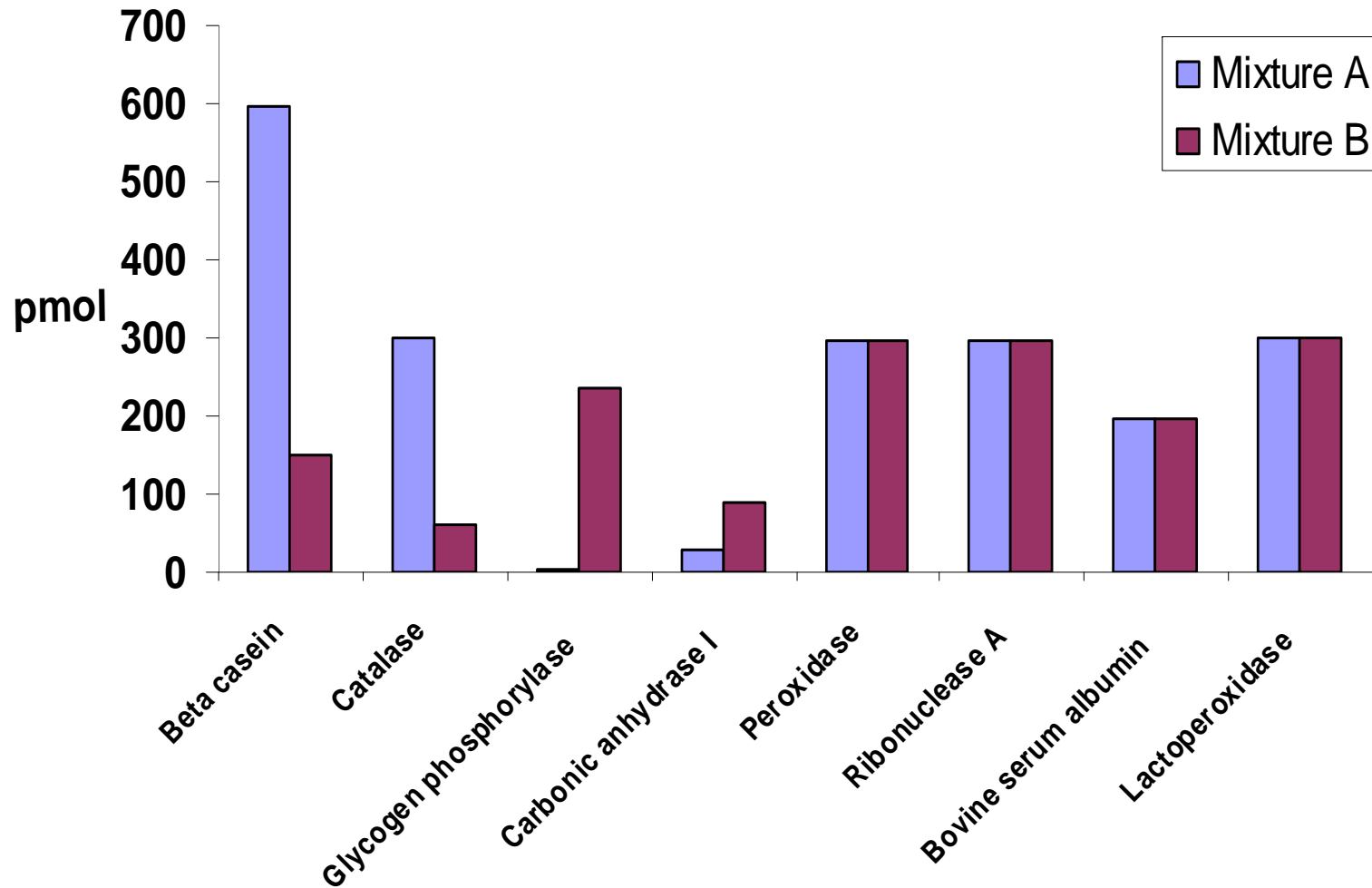
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- **Welche Methoden der relativen Quantifizierung werden verwendet?**
- **Wie erfolgreich sind die einzelnen Methoden?**
- **Wie sehr sind die Methoden in Labors etabliert?**
- **Wie geeignet ist Quantifizierungs Software?**
- **Confidence Level?**
- **Quantifizierungs Projekte routine?**



# PRG2006 Relative Quantifizierung

Probe



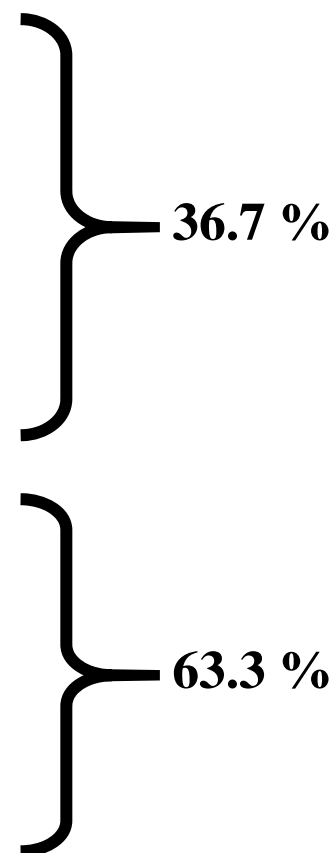


# PRG2006 Relative Quantifizierung

## Verwendete Methoden

### Quantifizierungsmethode Anzahl

1D Coomassie	3
2D Coomassie	4
2D silver	2
1D fluorescence	4
2D fluorescence	1
2D radioactivity	1
2D DIGE	3
Isotope ICPL	4
Isotope iTRAQ	11
Isotope O-methylisourea	1
Isotope $^{16}\text{O}^{18}\text{O}$	4
Spectral count	1
Ion current	9



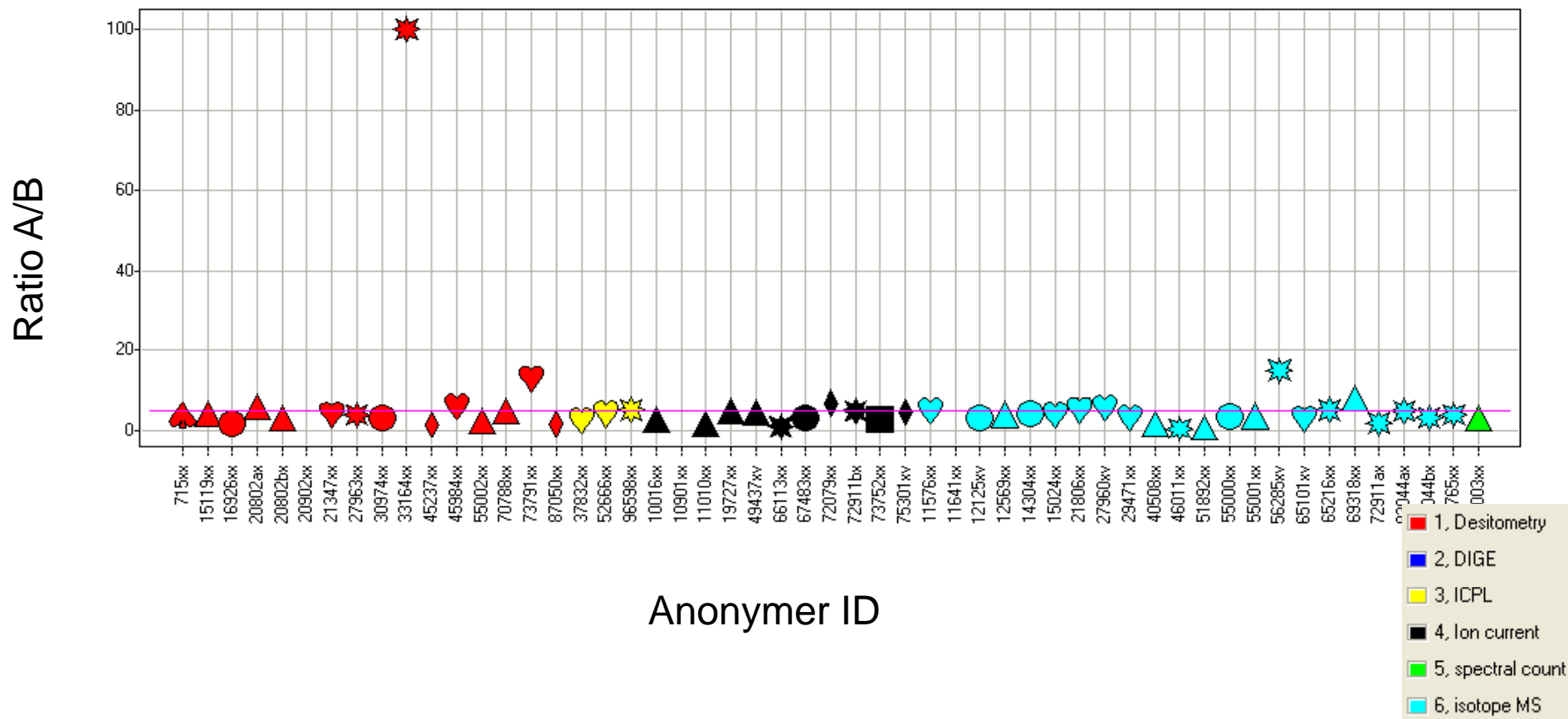


# PRG2006 Relative Quantifizierung

## Ergebnisse – Catalase (5:1)

Gel-basierte Methoden

Gel-freie Methoden



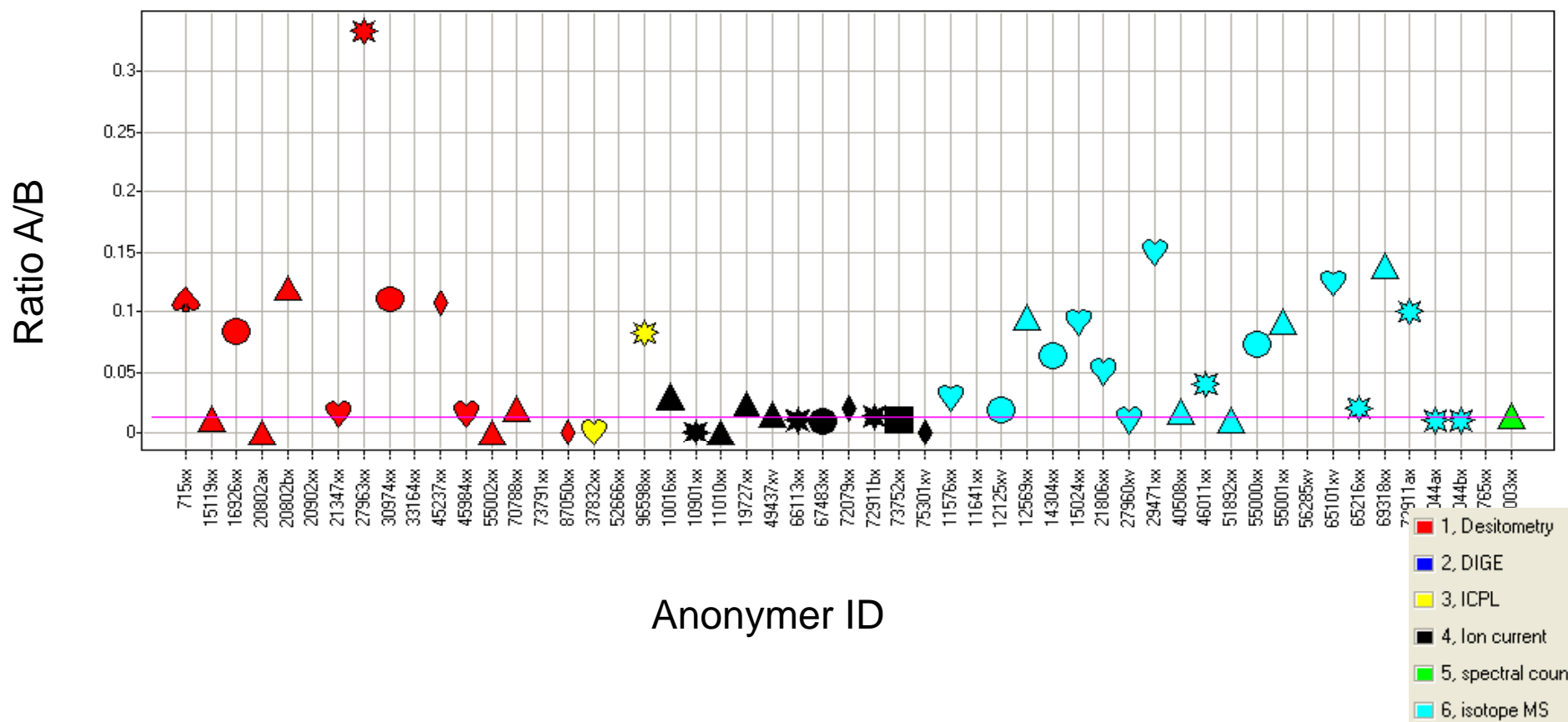


# PRG2006 Relative Quantifizierung

## Ergebnisse – Glycogen Phosphorylase (1:76)

Gel-basierte Methoden

Gel-freie Methoden





# *PRG2006 Relative Quantifizierung*

## *Ergebnisse*

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- **Erfolgsquote der einzelnen Methoden?**
  - **Die größte “% Fehlerquote” wurde für Glycogen Phosphorylase (1:76) beobachtet.**
  - **Insgesamt zeigte die Elektrophorese größere “% Fehlerquote” als die auf Massenspektrometrie basierenden Methoden.**
  - **‘Ion Current’ und ‘Spectral Count’ waren genau so erfolgreich wie die auf ‘Stable Isotope Labeling’ basierten Methoden.**



# *PRG2009 Research Study*

*Relative Quantifizierung in einer klinischen Matrix*

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# *PRG2011 Survey Study*

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## **Interaktion zwischen Cores und Klienten**





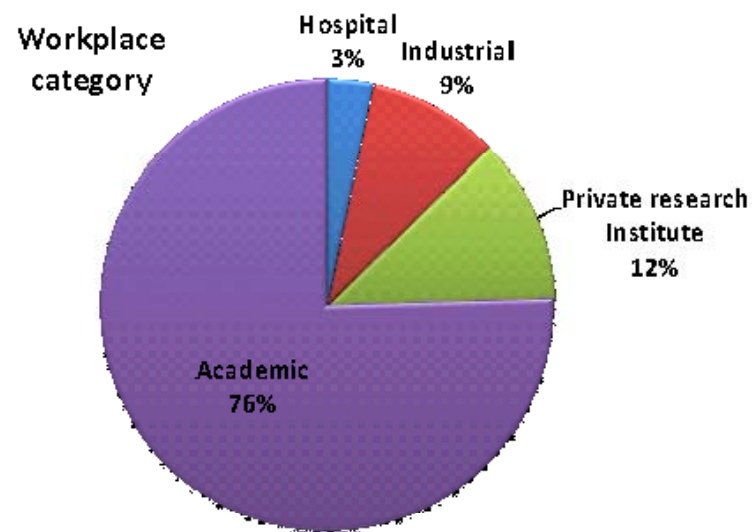
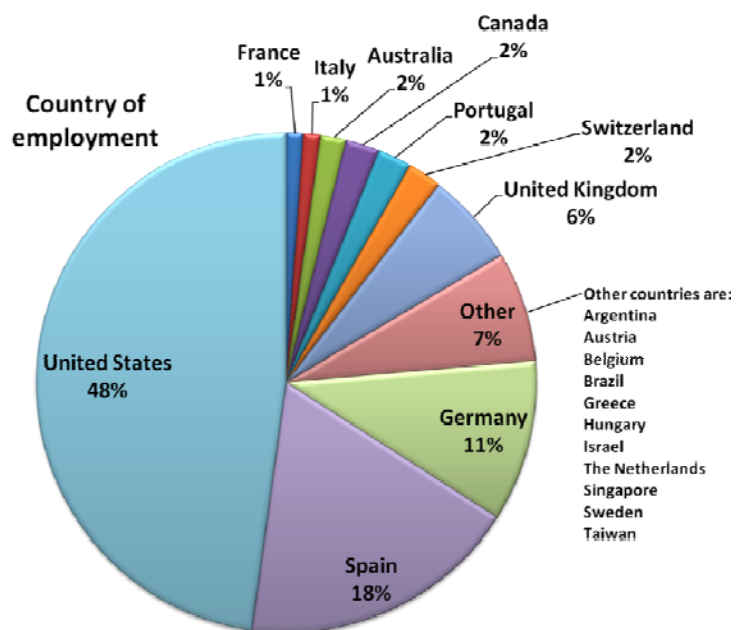
## *PRG2011 Survey Ziele*

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- **Finanzierung**
- **Technologie Trends**
- **Anwender Wünsche**
- **Kommunikation Cores und Klienten**

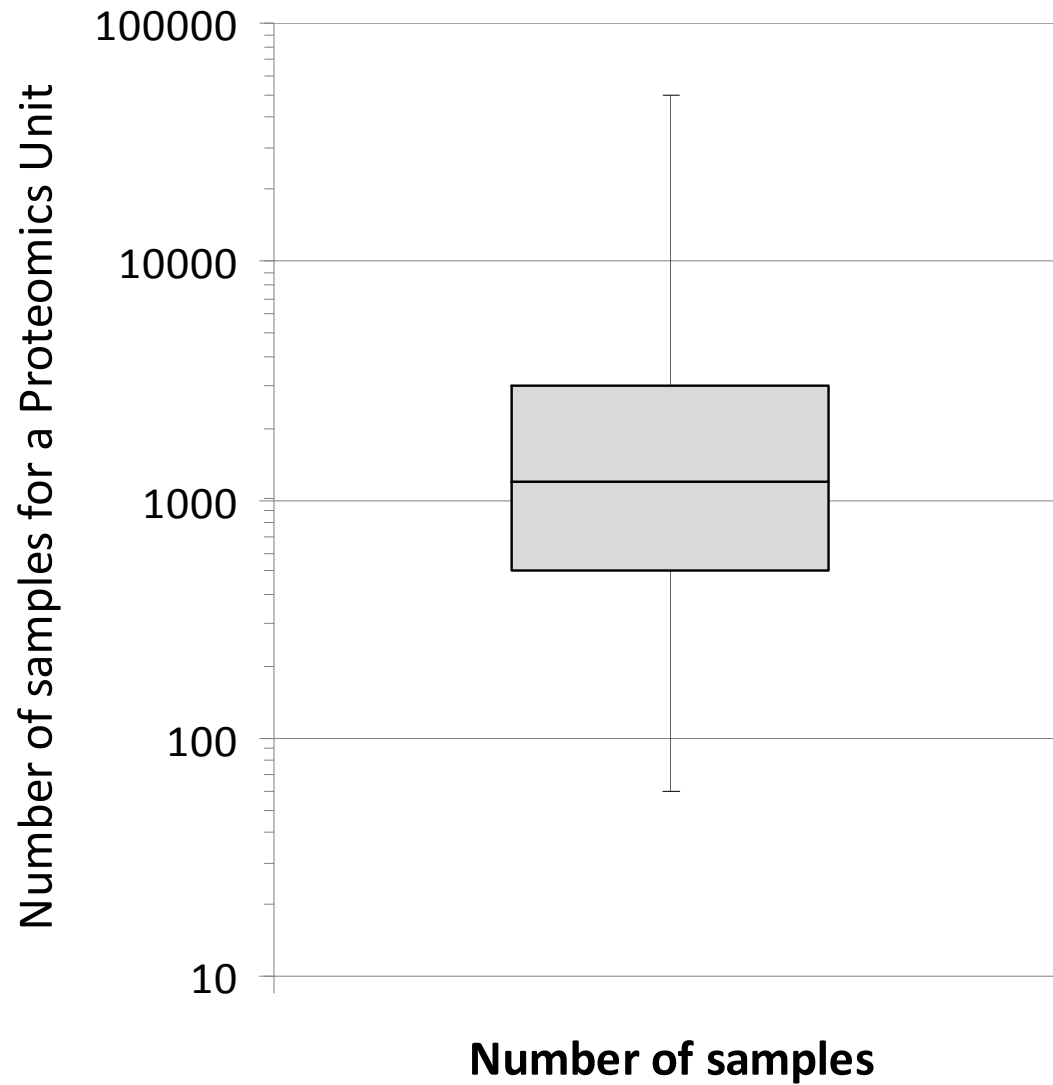


# Demographie



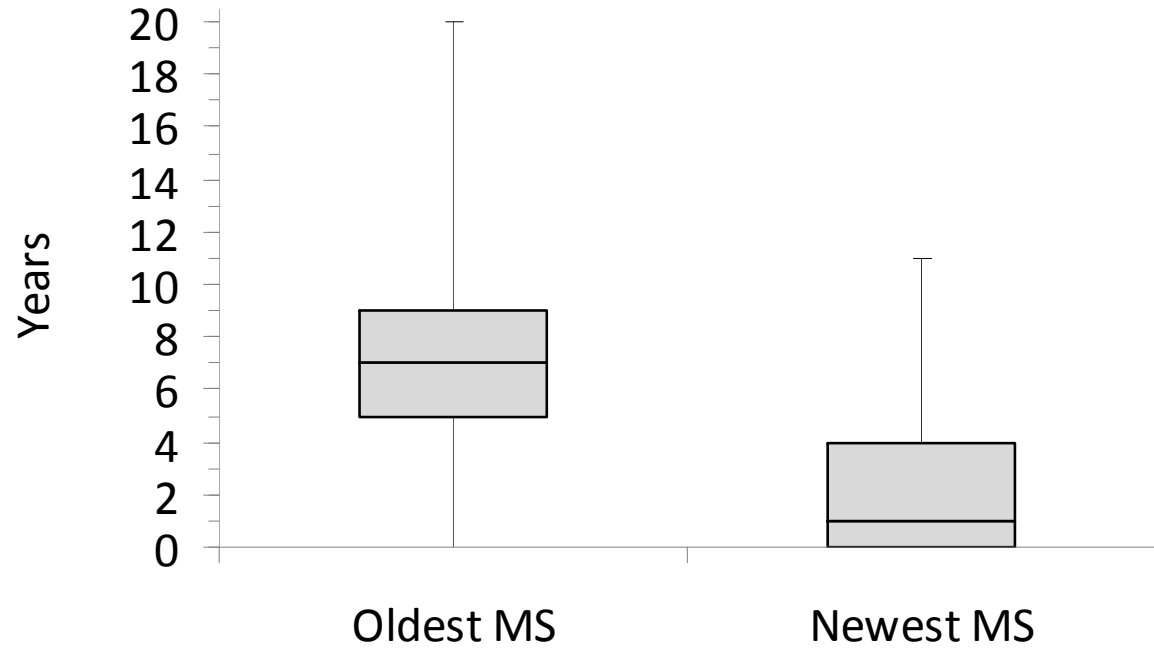
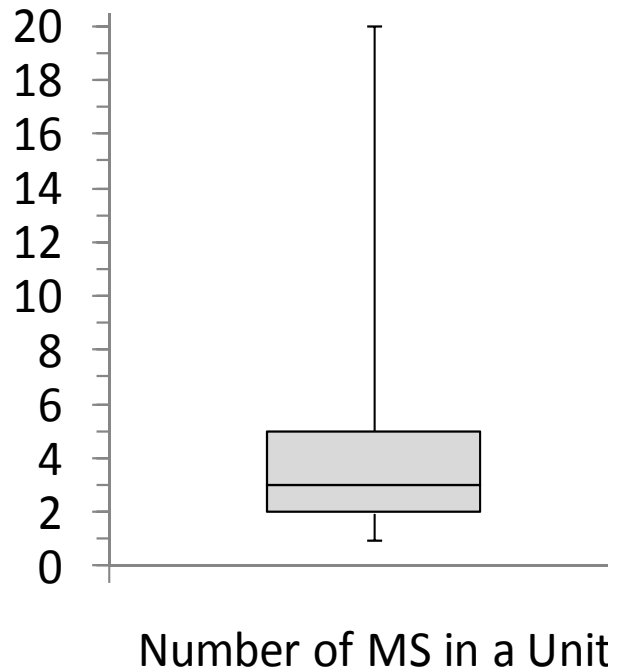


# *Anzahl Proben pro Jahr*



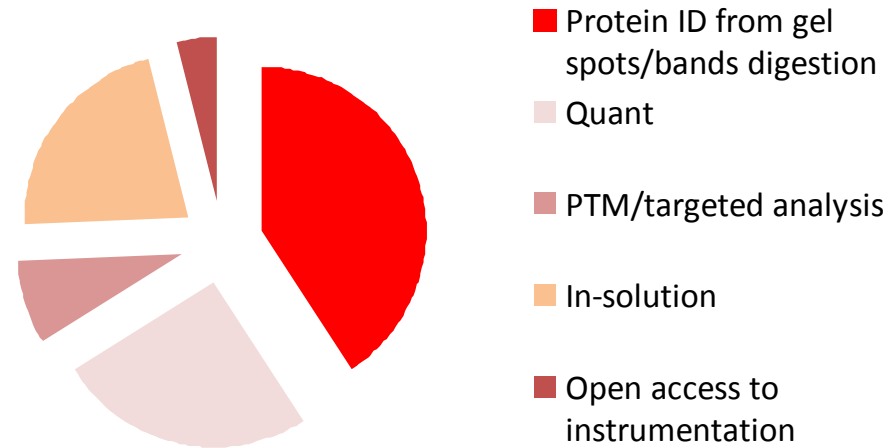


# *Massenspektrometer*

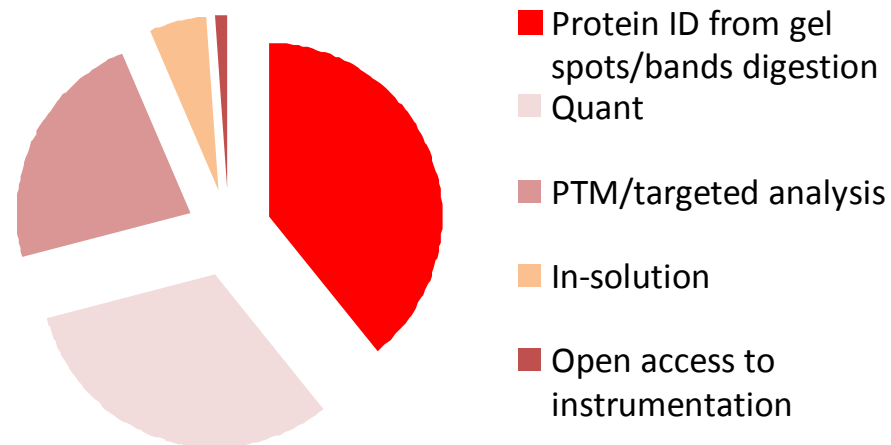


# Projekte

## As seen from Unit



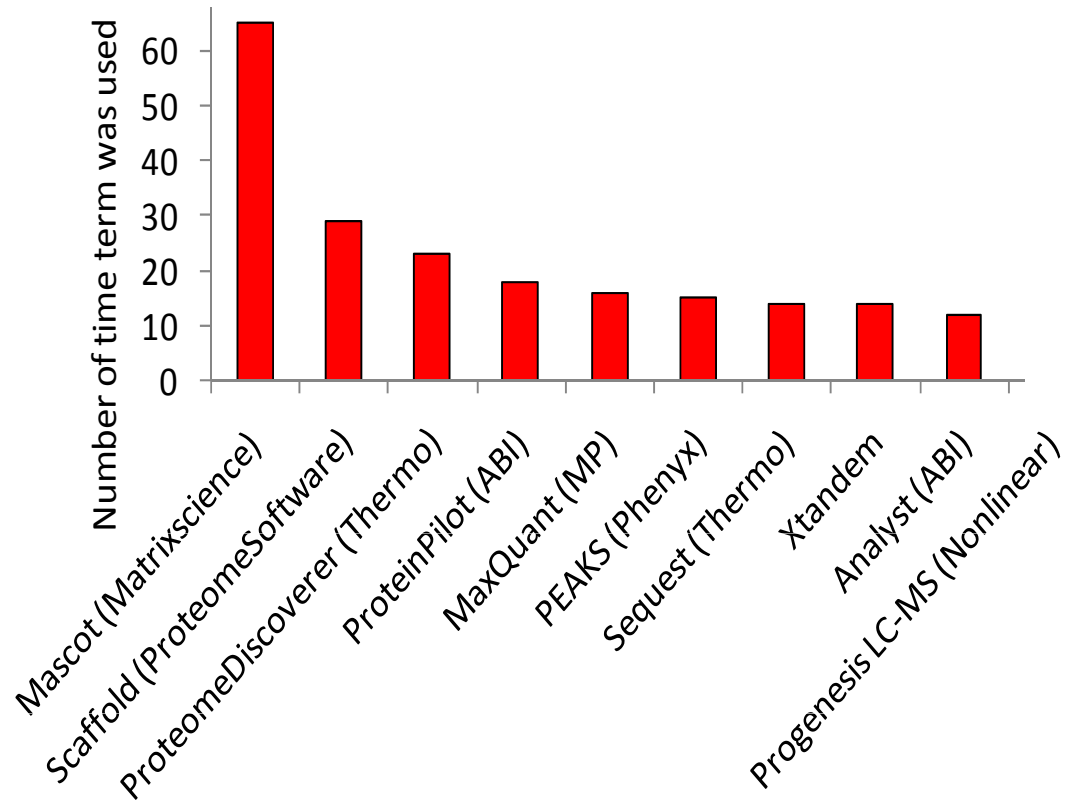
## As seen from user



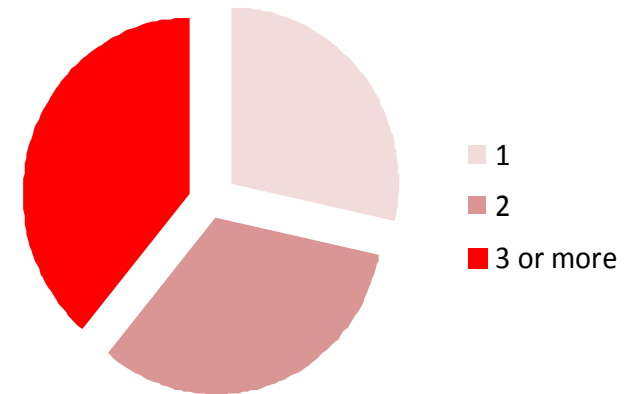


# Software

### 10 most used Software

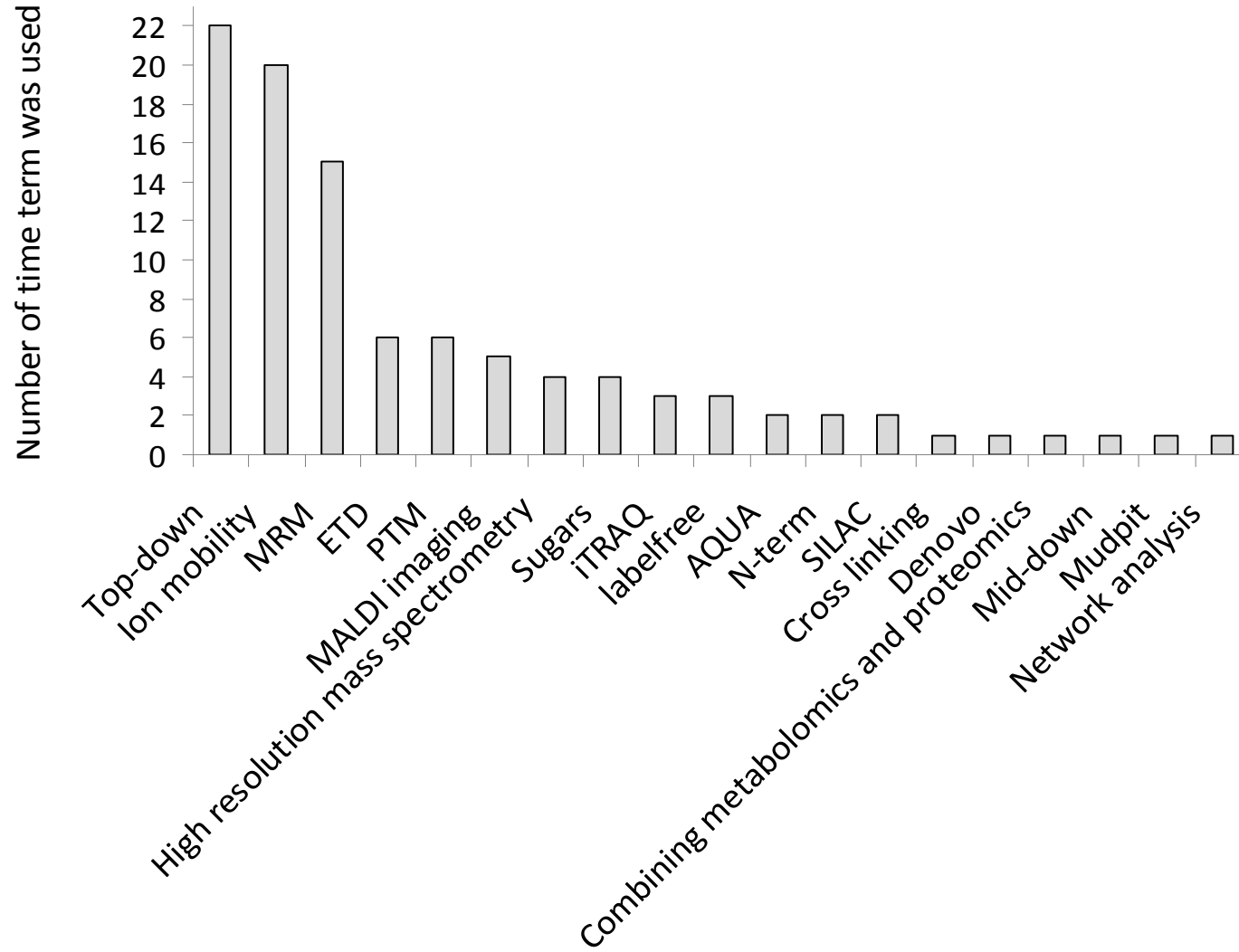


### Number of search algorithms used in a facility





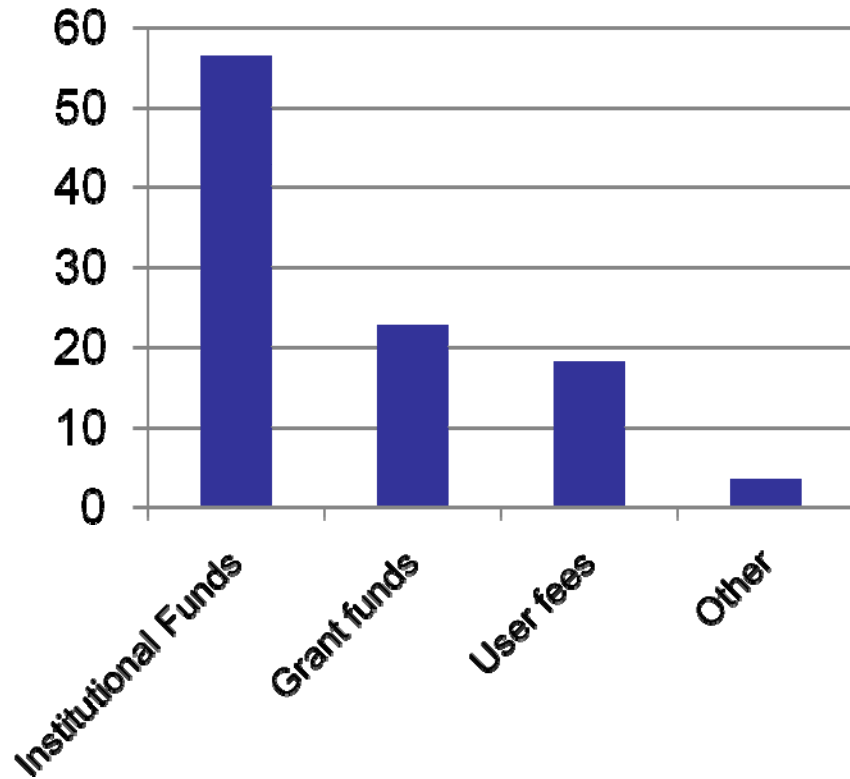
# Technologie Wunschliste



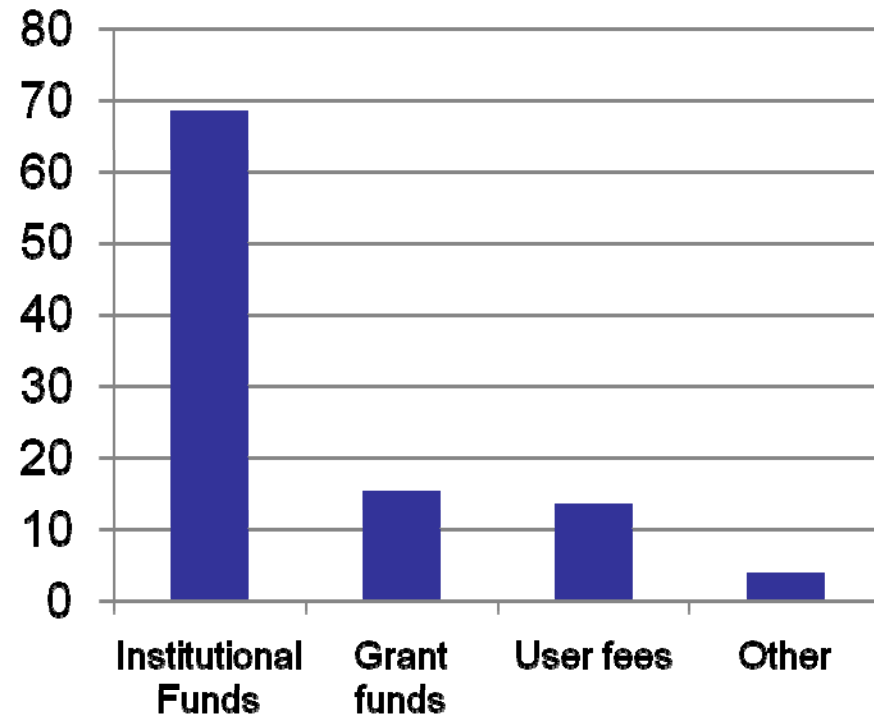


# Finanzierung Personal

### Overall contribution to funding personnel



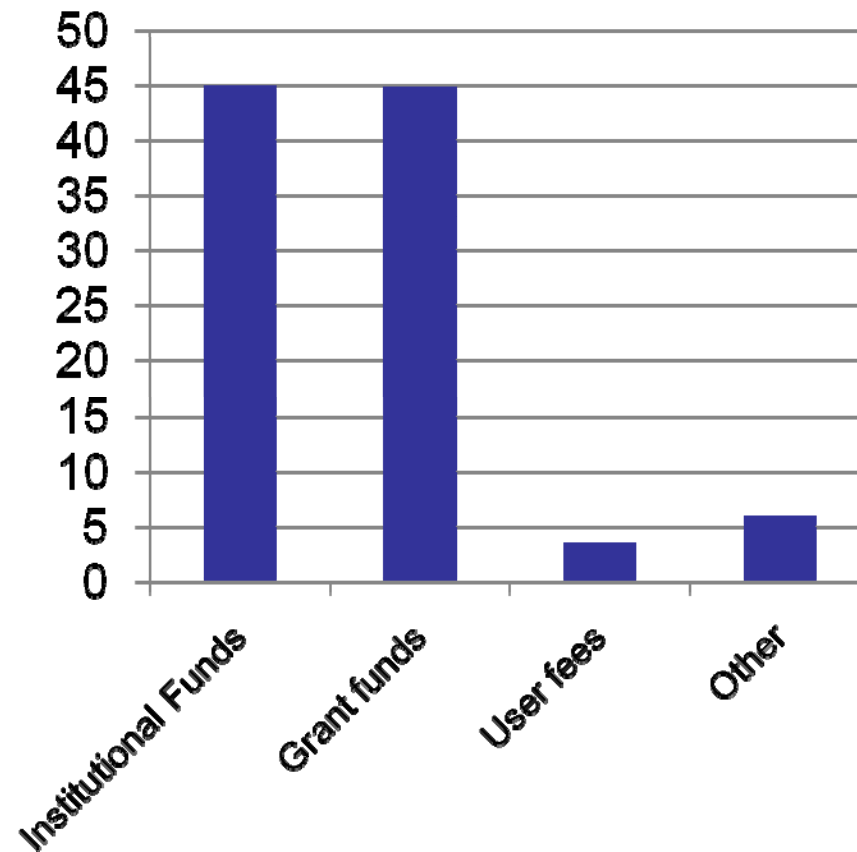
### Overall contribution to funding the director





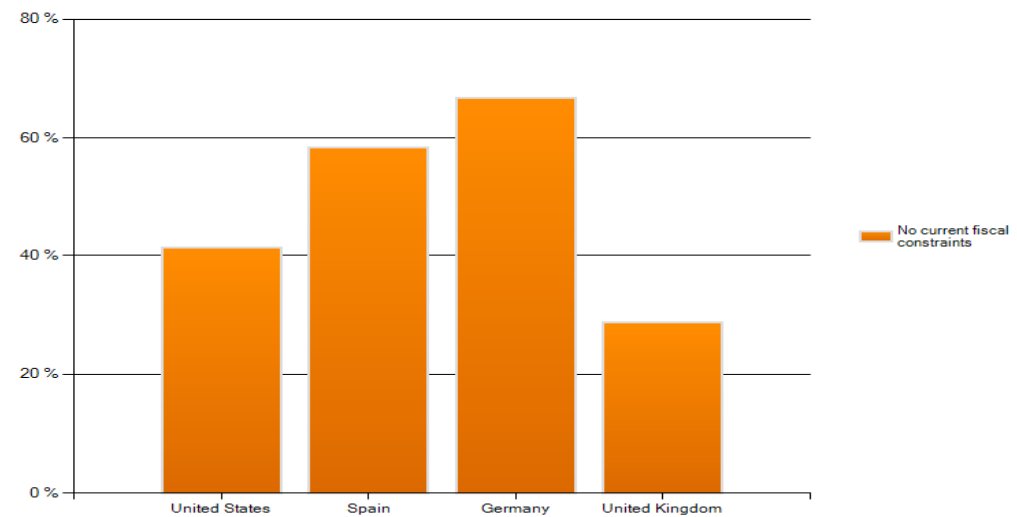
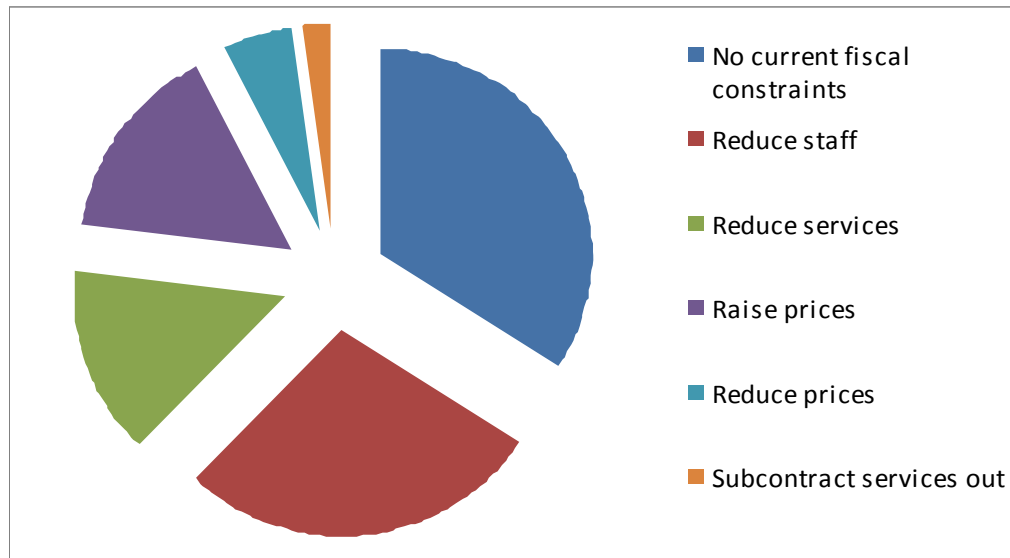
# *Finanzierung Geräte*

**Overall contribution to funding instrumentation**



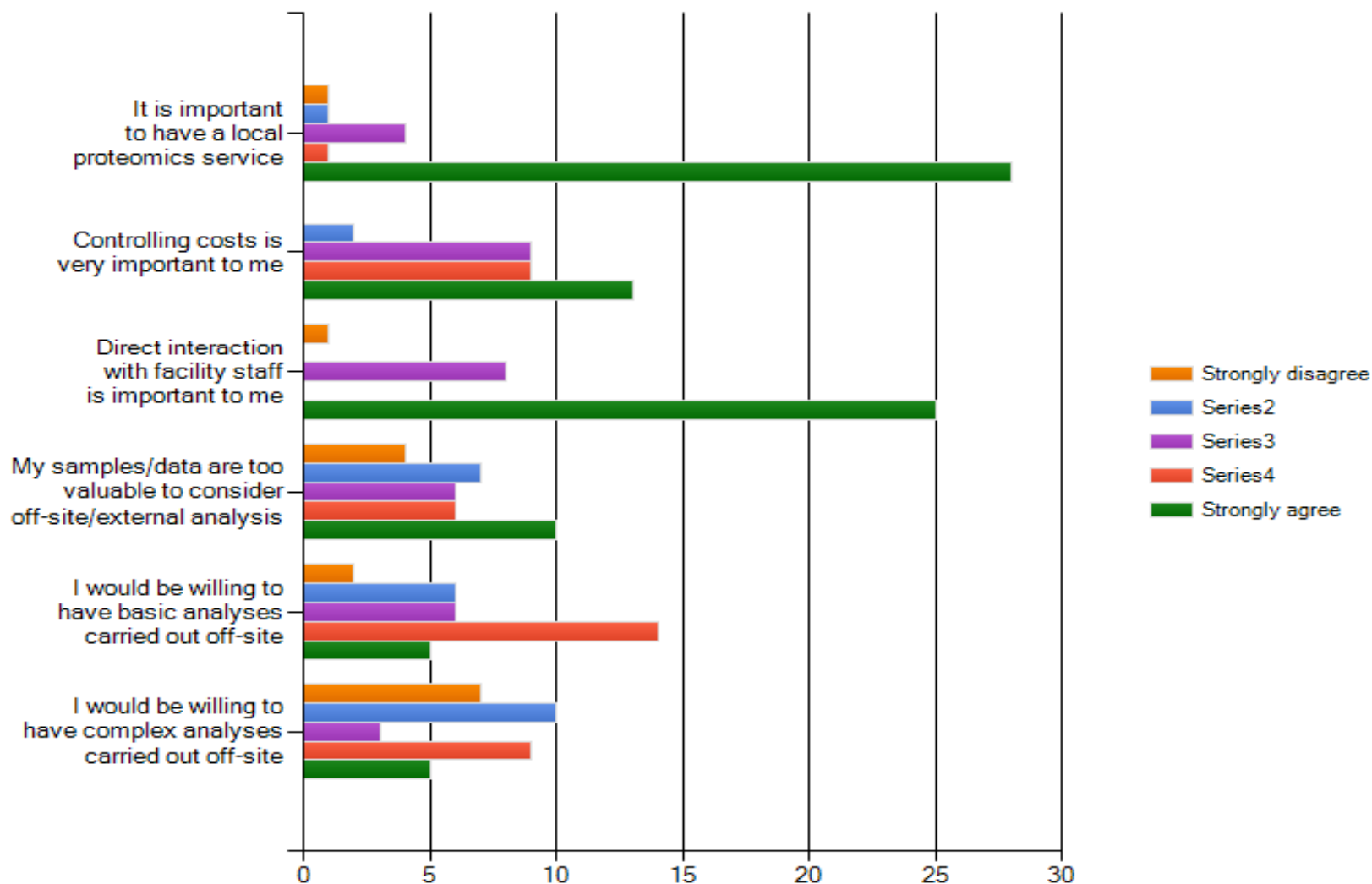


# Finanzielle Engpässe - was tun?





## *Lokales vs. externes Labor*





## *Acknowledgements*

**The Proteomics Research Group gratefully acknowledges the ABRF and the Executive Board for their generous support. Special thanks to all the study participants.**

***Thank You!***